



SEQUENCE LISTING

<110> Hoogenboom Hendricus R.J.M.
Hendrikx, Maria P.G.

<120> MUCIN-1 Specific Binding Members and Methods of Use Thereof

<130> DYX-015.1 US

<140> 09/822,698

<141> 2001-03-30

<150> US 09/538,913

<151> 2000-03-30

<160> 112

<170> Microsoft Word

<210> 1

<211> 113

<212> PRT

<213> artificial sequence

<220>

<223> light chain variable region of the MUC1-specific
binding domain of PH1 Fab antibody

<400> 1

Glu Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
85 90 95

Leu Gln Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105 110

Arg

<210> 2

<211> 339

<212> DNA

<213> artificial sequence

<220>

<223> nucleotide sequence coding for amino acid sequence of
SEQ ID NO:1

<400> 2

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gaaattgtgc tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc      60
atctcctgca ggtctagtca gagcctcctg catagtaatg gatacaccta tttggattgg      120
tacctgcaga agccagggca gtctccacag ctctgatct attcgggttc tcatcggggc      180
tccgggggtcc ctgacagggt cagtggcagt gtatcaggca cagattttac actgagaatc      240
agcagagtgg aggctgagga tgttgagatt tattactgca tgcagggtct acagagtcca      300
ttcactttcg gccctgggac caaagtggat atcaaacga                               339
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<210> 3

<211> 121

<212> PRT

<213> artificial sequence

<220>

<223> heavy chain variable region of the MUC1-specific
binding domain of the PH1 Fab antibody

<400> 3

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Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1           5           10           15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Asn
          20           25           30

Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35           40           45

Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
          50           55           60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65           70           75           80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
          85           90           95

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly
          100          105          110

Gln Gly Thr Leu Val Thr Val Ser Ser
          115          120
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<210> 4
 <211> 363
 <212> DNA
 <213> artificial sequence

 <220>
 <223> nucleotide sequence coding for amino acid sequence of
 SEQ ID NO:3

 <400> 4

 caggtccagc tgggtgcagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt cacgtttaga agtaacgcca tgggctgggt ccgccaggct 120
 ccaggggaagg ggctggagtg ggtctcaggt attagtggta gtggtggcag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgag agccgaggac acggccgtat attattgtgc gaaacatacc 300
 gggggggggtc tttgggaccc cattgactac tggggccagg gaaccctggt caccgtctca 360
 agc 363

<210> 5
 <211> 381
 <212> PRT
 <213> artificial sequence

 <220>
 <223> MUC1-specific immunocytokine bivPH1-IL-2

 <400> 5

 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Asn
 20 25 30
 Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly
 100 105 110

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Ala	Leu	Glu	Ile	115	120	125
Val	Leu	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Thr	Pro	Gly	Glu	Pro	130	135	140
Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser	Asn	Gly	145	150	155
Tyr	Thr	Tyr	Leu	Asp	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Gln	165	170	175
Leu	Leu	Ile	Tyr	Ser	Gly	Ser	His	Arg	Ala	Ser	Gly	Val	Pro	Asp	Arg	180	185	190
Phe	Ser	Gly	Ser	Val	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Arg	Ile	Ser	Arg	195	200	205
Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	Gly	Leu	Gln	210	215	220
Ser	Pro	Phe	Thr	Phe	Gly	Pro	Gly	Thr	Lys	Val	Asp	Ile	Lys	Arg	Gly	225	230	235
Gly	Gly	Ser	Gly	Gly	Gly	Ala	Leu	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys	245	250	255
Lys	Thr	Gln	Leu	Gln	Leu	Glu	His	Leu	Leu	Leu	Asp	Leu	Gln	Met	Ile	260	265	270
Leu	Asn	Gly	Ile	Asn	Asn	Tyr	Lys	Asn	Pro	Lys	Leu	Thr	Arg	Met	Leu	275	280	285
Thr	Phe	Lys	Phe	Tyr	Met	Pro	Lys	Lys	Ala	Thr	Glu	Leu	Lys	His	Leu	290	295	300
Gln	Cys	Leu	Glu	Glu	Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	305	310	315
Ala	Gln	Ser	Lys	Asn	Phe	His	Leu	Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	325	330	335
Ile	Asn	Val	Ile	Val	Leu	Glu	Leu	Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	340	345	350
Cys	Glu	Tyr	Ala	Asp	Glu	Thr	Ala	Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg	355	360	365
Trp	Ile	Thr	Phe	Cys	Gln	Ser	Ile	Ile	Ser	Thr	Leu	Thr				370	375	380

<210> 6
 <211> 1143
 <212> DNA
 <213> artificial sequence

Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly
 1 5 10 15
 Ser Thr Ala Pro
 20

<210> 8
 <211> 20
 <212> PRT
 <213> artificial sequence

 <220>
 <223> peptide of MUC1 protein

 <400> 8

Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro
 1 5 10 15

 Pro Ala His Gly
 20

<210> 9
 <211> 24
 <212> DNA
 <213> artificial sequence

 <220>
 <223> CH1FOR primer

 <400> 9

gtccttgacc aggcagccca gggc 24

<210> 10
 <211> 23
 <212> DNA
 <213> artificial sequence

 <220>
 <223> pUC-reverse primer

 <400> 10

agcggataac aatttcacac agg 23

<210> 11
 <211> 44
 <212> DNA
 <213> artificial sequence

 <220>
 <223> VL backward primer

<400> 11

accgcctcca ccagtcgact tgaaattgtg ctgactcagt ctcc 44

<210> 12

<211> 51

<212> DNA

<213> artificial sequence

<220>

<223> VL forward primer

<400> 12

accgcctcca ccgggcgcgc cttattaaca ctctcccctg ttgaagctct t 51

<210> 13

<211> 61

<212> DNA

<213> artificial sequence

<220>

<223> VL backward primer for light chain variable region
of the PH1 Fab antibody with additional linker and
restriction sites

<400> 13

gccgatcgct ctggtcaccg tctcaagcgg aggcggtgca cttgaaattg tgctgactca 60

g 61

<210> 14

<211> 50

<212> DNA

<213> artificial sequence

<220>

<223> VL forward primer for light chain variable region
of PH1 Fab antibody with additional linker and
restriction sites

<400> 14

gtctcgcgag cggccgccga ttggatatcc actttggtcc cagggccgaa 50

<210> 15

<211> 27

<212> DNA

<213> artificial sequence

<220>

<223> nucleotide sequence coding for a

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          nine amino acid linker

<400> 15

gggggtggat caggcggcgg ggccta                27

<210> 16
<211> 69
<212> DNA
<213> artificial sequence

<220>
<223> PH1-IL-2 backward primer

<400> 16

accaaagtgg atatcaaacg aggggggtgga tcaggcggcg gggccctagc acctacttca        60

agttctaca                                     69

<210> 17
<211> 49
<212> DNA
<213> artificial sequence

<220>
<223> PH1-IL-2 forward primer

<400> 17

gtcccgcgtg cggccgcagt cagtgttgag atgatgcttt gacaaaagg                49

<210> 18
<211> 98
<212> PRT
<213> artificial sequence

<220>
<223> heavy chain variable region from a DP47 germ line

<400> 18

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
          20          25          30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35          40          45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
          50          55          60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys

<210> 19
<211> 100
<212> PRT
<213> artificial sequence

<220>
<223> light chain variable region from a DPK 15 germ line

<400> 19

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

Leu Gln Thr Pro
100

<210> 20
<211> 14
<212> PRT
<213> artificial sequence

<220>
<223> myc tag peptide

<400> 20

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
1 5 10

<210> 21
<211> 42

109020"3532350

<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence coding for amino acid sequence
of SEQ ID NO:20

<400> 21
gaacaaaaac tcattctcaga agaggatctg aatggggccg ca

42

<210> 22
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> hexahistidine peptide

<400> 22

His His His His His His
1 5

<210> 23
<211> 18
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence coding for amino acid sequence
of SEQ ID NO:22

<400> 23
catcaccatc atcaccat

18

<210> 24
<211> 220
<212> PRT
<213> artificial sequence

<220>
<223> immunoglobulin kappa light chain of MUC1-specific PH1-IgG1

<400> 24

Glu Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35	40	45
Pro Gln Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro		
50	55	60
Asp Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile		
65	70	75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly		
	85	90 95
Leu Gln Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys		
	100	105 110
Arg Gly Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp		
	115	120 125
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn		
	130	135 140
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu		
	145	150 155 160
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp		
	165	170 175
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr		
	180	185 190
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser		
	195	200 205
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys		
	210	215 220

<210> 25
 <211> 663
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for amino acid sequence of
 SEQ ID NO:24

<400> 25

gaaattgtgc tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc	60
atctcctgca ggtctagtca gagcctcctg catagtaatg gatacaccta tttggattgg	120
tacctgcaga agccagggca gtctccacag ctctgatct attcgggttc tcatcggggc	180
tccgggggtcc ctgacaggtt cagtggcagt gtatcaggca cagattttac actgagaatc	240
agcagagtgg aggctgagga tggtggagtt tattactgca tgcagggtct acagagtcca	300

ttcacttttcg gccctgggac caaagtggat atcaaacgag gaactgtggc tgcaccatct 360
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540
ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600
gaagtcaccc atcagggcct gagttcaccg gtgacaaaga gcttcaacag gggagagtgt 660
tag 663

<210> 26
<211> 451
<212> PRT
<213> artificial sequence

<220>
<223> immunoglobulin heavy chain of MUC1-specific PH1-IgG1

<400> 26

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Asn
20 25 30
Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

[illegible]

<210> 28
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <221> variant
 <222> (1)..(14)
 <223> amino acid positions designated Xaa may be varied
 to form alternative regions of a MUC1-specific
 binding member as explained in the disclosure

 <400> 28

Xaa Xaa His Thr Gly Xaa Gly Val Trp Xaa Pro Xaa Xaa Xaa
 1 5 10

<210> 29
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <223> region of a MUC1-specific binding member

 <400> 29
 Ala Lys His Thr Gly Arg Gly Val Trp Asp Pro Ile Gly Tyr
 1 5 10

<210> 30
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <223> region of a MUC1-specific binding member

 <400> 30
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Lys His
 1 5 10

<210> 31
 <211> 14
 <212> PRT
 <213> artificial sequence

 <220>
 <223> region of a MUC1-specific binding member

 <400> 31
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr

1

5

10

<210> 32
 <211> 14
 <212> PRT
 <213> artificial sequence

<220>
 <223> amino acid sequence in a MUC1-specific binding member
 <400> 32

Ala Ile His Thr Gly Gly Gly Val Trp Asp Pro Ile Lys Tyr
 1 5 10

<210> 33
 <211> 33
 <212> DNA
 <213> artificial sequence

<220>
 <221> misc_feature
 <222> (1)..(33)
 <223> n may be varied according to the disclosure
 to form mutagenic primer sequences

<400> 33
 ggattcacgt ttagannnaa cgccatgggc tgg

33

<210> 34
 <211> 39
 <212> DNA
 <213> artificial sequence

<220>
 <221> misc_feature
 <222> (1)..(39)
 <223> n may be varied according to the disclosure
 to form mutagenic primer sequences

<400> 34

cacggagtct gcgtannntg tnnngccacc actaccact

39

<210> 35
 <211> 90
 <212> DNA
 <213> artificial sequence

<220>
 <221> misc_feature
 <222> (1)..(90)

<223> n may be varied according to the disclosure
to form mutagenic primer sequences

<400> 35

ctatgagacg gtgaccaggg ttccctggcc ccannnnnnn nnnnnnnnnn nnnnnnnnnn 60

nnnnnnnnnn nnnnnnacaat aatatacggc 90

<210> 36

<211> 90

<212> DNA

<213> artificial sequence

<220>

<221> misc_feature

<222> (1)..(90)

<223> n may be varied according to the disclosure
to form mutagenic primer sequences

<400> 36

ctatgagacg gtgaccaggg ttccctggcc ccagtagtca atgggggtccc aaacmnnmnn 60

mnnmnnmnnnt ttcgcacaat aatatacggc 90

<210> 37

<211> 90

<212> DNA

<213> artificial sequence

<220>

<221> misc_feature

<222> (1)..(90)

<223> n may be varied according to the disclosure
to form mutagenic primer sequences

<400> 37

ctatgagacg gtgaccaggg ttccctggcc ccagtagtcm nnnnnnnnnn nnnngccccc 60

cccggatatgt ttcgcacaat aatatacggc 90

<210> 38

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> HuJH4-5-FOR primer

<400> 38

tgaggagacg gtgaccaggg ttcc 24

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

<210> 47
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <221> variant
 <222> (1)..(16)
 <223> Xaa, designated as "&" in the disclosure, indicates end
 of amino acid sequence because mutation in nucleotide
 sequence forms a translational stop codon

<400> 47

Ala Lys Xaa His Thr Lys Thr Val Trp Asp Pro Ile Asp Tyr Trp Gly
 1 5 10 15

<210> 48
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 48

gcgaaatagc atacgaagac ggtttgggac cccattgact actggggc 48

<210> 49
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

<400> 49

Ala Lys Ile Thr Val Ser Arg Val Trp Asp Pro Ile Asp Tyr Trp Gly
 1 5 10 15

<210> 50
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 50

gcgaaaatta ctgtagtcg tgtttgggac cccattgact actggggc 48

109020-259320

<210> 51
<211> 16
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 51

Ala Lys Arg Tyr Leu Tyr Asp Val Trp Asp Pro Ile Asp Tyr Trp Gly
1 5 10 15

<210> 52
<211> 48
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence coding for a mutant CDR3 region

<400> 52

gcgaaacgtt atctgtatga tgtttgggac cccattgact actggggc 48

<210> 53
<211> 16
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 53

Ala Lys His Thr Gly Gly Gly Thr Leu Gln Arg Leu Asp Tyr Trp Gly
1 5 10 15

<210> 54
<211> 48
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence coding for a mutant CDR3 region

<400> 54

gcgaaacata cggggggggg cactttgcag cggctggact actggggc 48

<210> 55
<211> 16

<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 55

Ala	Lys	His	Thr	Gly	Gly	Gly	Thr	Gln	Thr	Pro	Cys	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 56
<211> 48
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence coding for a mutant CDR3 region

<400> 56

gcgaaacata ccggggggggg cactcagact ccgtgtgact actgggggc 48

<210> 57
<211> 16
<212> PRT
<213> artificial sequence

<220>
<223> mutant CDR3 region of an antibody heavy chain variable region

<400> 57

Ala	Lys	His	Thr	Gly	Gly	Gly	Arg	Arg	Ile	Cys	His	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 58
<211> 48
<212> DNA
<213> artificial sequence

<220>
<223> nucleotide sequence coding for a mutant CDR3 region

<400> 58

gcgaaacata ccggggggggg ccgtcgtatt tgatcatgact actgggggc 48

<210> 59
<211> 16
<212> PRT
<213> artificial sequence

<220>
 <221> variant
 <222> (1)..(16)
 <223> Xaa, designated as "&" in the disclosure, indicates end
 of amino acid sequence because mutation in nucleotide
 sequence forms a translational stop codon

<400> 59

Ala	Lys	His	Thr	Gly	Gly	Gly	Xaa	Arg	Xaa	Xaa	Arg	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 60
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 60

gcgaaacata ccggggggggg ctagcggtag tagcgggact actgggggc

48

<210> 61
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavychain variable region

<400> 61

Ala	Lys	His	Thr	Gly	Gly	Gly	Gln	Lys	Leu	Gln	Leu	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 62
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 62

gcgaaacata ccggggggggg ccagaagctg cagctggact actgggggc

48

<210> 63
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <221> variant
 <222> (1)..(16)
 <223> Xaa, when designated as "&" in the disclosure, indicates end
 of amino acid sequence because mutation in nucleotide sequence
 forms a translational stop codon; or when designated as "s" in
 the disclosure, Xaa is serine

<400> 63

Ala	Xaa	His	Thr	Gly	Gly	Arg	Gly	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 64
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
 <223> nucleotide sequence coding for a mutant CDR3 region

<400> 64

gcgtsacata cgggggggcg cggttgggac cccattgact actggggc

48

<210> 65
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <223> mutant CDR3 region of an antibody heavy chain variable region

<400> 65

Ala	Asn	Gln	Thr	Gly	Gly	Gly	Val	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 66
 <211> 48
 <212> DNA
 <213> artificial sequence

<220>
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48

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<212> PRT
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 <400> 69

Ala	Lys	Pro	Thr	Gly	Gly	Gly	Ala	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

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<400> 71

Ala Lys His Thr Gly Val Gly Val Trp His Pro Ile Tyr Tyr Trp Gly
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48

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<400> 73

Ala Lys His Thr Gly Val Gly Val Trp Asp Pro Ile Lys Tyr
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Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Lys
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Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Leu Asp Asn
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Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Tyr
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Ala Lys His Thr Gly Ser Gly Val Trp Asp Pro Ile Asn Tyr
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Thr Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Tyr
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Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Tyr
 1 5 10

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Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Asn
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<210> 91
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Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Phe Ala Tyr

1 5 10

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Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met Asp Tyr
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Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile His Tyr
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Ala Ile His Thr Gly Ala Gly Val Trp Asp Pro Ile Arg Tyr
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Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Val Tyr
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 <400> 107

Ala Gln His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr
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<210> 108
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<223> mutant CDR3 region of an antibody heavy chain variable region

Ala Lys His Thr Gly Arg Gly Val Trp Asp Pro Ile Asp Tyr
1 5 10

<211> 14

<213> artificial sequence

<223> mutant CDR3 region of an antibody heavy chain variable region

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<213> artificial sequence

<223> VKexpress-MUC-for primer

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<220>
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35

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